APPENDIX A
VERSIONS WITH MARKINGS TO SHOW CHANGES MADE

In the specification:

The paragraph beginning on page 22, line 16 was replaced with the following rewritten paragraph:

-- Two oligo DNA linkers, L1 (5'-GATCCCGGGTCACGTGGGAT-3') (SEQ ID NO:55) and L2 (5'-ATCCCACGTGACCCGG-3') (SEQ ID NO:56), were synthesized and phosphorylated by T4 polynucleotide kinase. After annealing of the both linkers, followed by ligation with the previously-prepared pSSD1 fragment by T4 DNA ligase, *Escherichia coli* JM109 was transformed. A plasmid pSSD3 was prepared from the transformant and the objective recombinant was confirmed by the determination of the base sequence of the linker-inserted fragment. Figure 1 illustrates the structure of the thus-obtained plasmid. The present plasmid vector carries three types of blunt-end formation restriction enzyme sites, SmaI, PmaCI, and EcoRV. Since these cleavage sites are positioned in succession at an interval of 7 bp, selection of an appropriate site in combination of three types of frames for the inserting cDNA allows to construct a vector expressing a fusion protein.--

The paragraph beginning on page 27, line 21 was replaced with the following rewritten paragraph:

-- The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the human α-2-HS-glycoprotein (SWISS-PROT Accession No. P02765). Table 4 indicates the comparison of the amino acid sequences between the human protein of the present invention (HP) (SEQ ID NO:1) and the human α-2-HS-glycoprotein (GP) (SEQ ID NO:57). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed a homology of 25.5%. The cysteine position is reserved and this region is analogous to that in cystatins (thiol proteinase inhibitors). There are observed other analogy with histidine-rich glycoprotein (P04196, 30.9%/194

amino acid residues), kininogen (P01045, 24.1%/261 amino acid residues), tyrosine kinase inhibitor (A32827, 24.4%/291 amino acid residues), and so on.--

The paragraph beginning on page 30, line 5 was replaced with the following rewritten paragraph:

-- The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the rat retinol dehydrogenase (NBRF Accession No. A55884). Table 5 indicates the comparison of the amino acid sequences between the human protein of the present invention (HP) (SEQ ID NO:2) and the rat retinol dehydrogenase (RN) (SEQ ID NO:58). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and. represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed a homology of 65.3% among the entire regions.--

The paragraph beginning on page 32, line 28 was replaced with the following rewritten paragraph:

-- The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the human HIV envelope glycoprotein gp120-binding C-type lectin (GenBank Accession No. M98457). Table 6 indicates the comparison of the amino acid sequences between the human protein of the present invention (HP) (SEQ ID NO:3) and the human HIV envelope glycoprotein gp120-binding C-type lectin (CL) (SEQ ID NO:59). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed a homology of 85.6% among 284 amino acid residues. There is observed at the downstream of the transmembrane domain a sequence with seven repetition of Ile-Tyr-Gln-Xaa-Leu-Thr-Xaa-Leu-Lys-Ala-Ala-Val-Gly-Glu-Leu-Xaa-Xaa-Xaa-Ser-Lys-Xaa-Gln-Xaa (SEQ ID NO:60).--

The paragraph beginning on page 35, line 20 was replaced with the following rewritten paragraph:

-- The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the human tumor-associated antigen L6 (SWISS-PROT Accession No. P30408). Table 7 indicates the comparison of the amino acid sequences between the human protein of the present invention (HP) (SEQ ID NO:4) and the human tumor-associated antigen L6 (L6) (SEQ ID NO:61). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed a homology of 47.0% among the entire regions.--

The paragraph beginning on page 37, line 20 was replaced with the following rewritten paragraph:

-- The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the mouse interstitial cell protein (GenBank Accession No. X96618). Table 8 indicates the comparison of the amino acid sequences between the human protein of the present invention (HP) (SEQ ID NO:5) and the mouse interstitial cell protein (MM) (SEQ ID NO:62). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed a homology of 79.6% among the entire regions.--

The paragraph beginning on page 39, line 19 was replaced with the following rewritten paragraph:

-- The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the nematode hypothetical protein F25D7.1 (GenBank Accession No. Z78418). Table 9 indicates the comparison of the amino acid sequences between the human protein of the present invention (HP) (SEQ ID NO:6) and the nematode hypothetical protein F25D7.1 (CE) (SEQ ID NO:63). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein

of the present invention. The both proteins possessed a homology of 49.8% among the entire regions.--

The paragraph beginning on page 43, line 6 was replaced with the following rewritten paragraph:

-- The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the nematode hypothetical protein of 28.5 kDa (SWISS-PROT Accession No. P34623). Table 10 indicates the comparison of the amino acid sequences between the human protein of the present invention (HP) (SEQ ID NO:9) and the nematode hypothetical protein of 28.5 kDa (CE) (SEQ ID NO:64). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed a homology of 42.8% in the C-terminal region of 243 amino acid residues.--

The paragraph beginning on page 45, line 17 was replaced with the following rewritten paragraph:

-- The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the swine steroidal membrane-binding protein (GenBank Accession No. X99714). Table 11 indicates the comparison of the amino acid sequences between the human protein of the present invention (HP) (SEQ ID NO:10) and the swine steroidal membrane-binding protein (SS) (SEQ ID NO:65). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed a homology of 96.4% among the entire regions.--

The paragraph beginning on page 47, line 5 was replaced with the following rewritten paragraph:

-- The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the cytochrome P450 as